

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti
Corley, Neil C.
Tang, Y. Tom
- (ii) TITLE OF THE INVENTION: AUTOANTIGEN-LIKE PROTEIN
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0385 US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: HUVENOB01
(B) CLONE: 35842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Phe	Pro	Arg	Val	Ser	Thr	Phe	Leu	Pro	Leu	Arg	Pro	Leu	Ser	Arg	
1				5				10					15			
His	Pro	Leu	Ser	Ser	Gly	Ser	Pro	Glu	Thr	Ser	Ala	Ala	Ala	Ile	Met	
			20					25					30			
Leu	Leu	Thr	Val	Arg	His	Gly	Thr	Val	Arg	Tyr	Arg	Ser	Ser	Ala	Leu	
			35				40					45				
Leu	Ala	Arg	Thr	Lys	Asn	Asn	Ile	Gln	Arg	Tyr	Phe	Gly	Thr	Asn	Ser	
	50					55					60					
Val	Ile	Cys	Ser	Lys	Lys	Asp	Lys	Gln	Ser	Val	Arg	Thr	Glu	Glu	Thr	
65					70					75					80	
Ser	Lys	Glu	Thr	Ser	Glu	Ser	Gln	Asp	Ser	Glu	Lys	Glu	Asn	Thr	Lys	
			85					90					95			
Lys	Asp	Leu	Leu	Gly	Ile	Ile	Lys	Gly	Met	Lys	Val	Glu	Leu	Ser	Thr	
			100					105					110			
Val	Asn	Val	Arg	Thr	Thr	Lys	Pro	Pro	Lys	Arg	Arg	Pro	Leu	Lys	Ser	
			115					120				125				
Leu	Glu	Ala	Thr	Leu	Gly	Arg	Leu	Arg	Arg	Ala	Thr	Glu	Tyr	Ala	Pro	
	130					135						140				
Lys	Lys	Arg	Ile	Glu	Pro	Leu	Ser	Pro	Glu	Leu	Val	Ala	Ala	Ala	Ser	
	145				150					155					160	
Ala	Val	Ala	Asp	Ser	Leu	Pro	Phe	Asp	Lys	Gln	Thr	Thr	Lys	Ser	Glu	
			165					170						175		
Leu	Leu	Ser	Gln	Leu	Gln	Gln	His	Glu	Glu	Glu	Ser	Arg	Ala	Gln	Arg	
			180					185					190			
Asp	Ala	Lys	Arg	Pro	Lys	Ile	Ser	Phe	Ser	Asn	Ile	Ile	Ser	Asp	Met	
			195					200					205			
Lys	Val	Ala	Arg	Ser	Ala	Thr	Ala	Arg	Val	Arg	Ser	Arg	Pro	Glu	Leu	
			210			215					220					
Arg	Ile	Gln	Phe	Asp	Glu	Gly	Tyr	Asp	Asn	Tyr	Pro	Gly	Gln	Glu	Lys	
	225				230					235				240		
Thr	Asp	Asp	Leu	Lys	Lys	Arg	Lys	Asn	Ile	Phe	Thr	Gly	Lys	Arg	Leu	
			245					250					255			
Asn	Ile	Phe	Asp	Met	Met	Ala	Val	Thr	Lys	Glu	Ala	Pro	Glu	Thr	Asp	
			260					265					270			
Thr	Ser	Pro	Ser	Leu	Trp	Asp	Val	Glu	Phe	Ala	Lys	Gln	Leu	Ala	Thr	
			275				280					285				
Val	Asn	Glu	Gln	Pro	Leu	Gln	Asn	Gly	Phe	Glu	Glu	Leu	Ile	Gln	Trp	
			290				295					300				
Thr	Lys	Glu	Gly	Lys	Leu	Trp	Glu	Phe	Pro	Ile	Asn	Asn	Glu	Ala	Gly	
			305		310					315				320		
Phe	Asp	Asp	Asp	Gly	Ser	Glu	Phe	His	Glu	His	Ile	Phe	Leu	Glu	Lys	
			325							330				335		
His	Leu	Glu	Ser	Phe	Pro	Lys	Gln	Gly	Pro	Ile	Arg	His	Phe	Met	Glu	
			340					345					350			
Leu	Val	Thr	Cys	Gly	Leu	Ser	Lys	Asn	Pro	Tyr	Leu	Ser	Val	Lys	Gln	
			355				360					365				
Lys	Val	Glu	His	Ile	Glu	Trp	Phe	Arg	Asn	Tyr	Phe	Asn	Glu	Lys	Lys	
			370			375					380					
Asp	Ile	Leu	Lys	Glu	Ser	Asn	Ile	Gln	Phe	Asn						
385					390					395						

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: HUVENOB01
 (B) CLONE: 35842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GACGTGTTTG	GCACGGGGAC	GCACCATTTT	AGTTGTGTTT	TTGGTTTCATT	TCGTGICTCG	60
GCAGATGTTTC	CTAGAGTCTC	GACGTTCCCTA	CCTCTTCGCC	CCCTTCCCG	CCACCCTTTG	120
TCCTCTGGAA	GCCCGGAGAC	ATCAGCGCGT	GCAGTTATGC	TACTCACTGT	TCGGCACGGA	180
ACAGTCAGGT	ACCGCAGTTC	AGCGCTGTTG	GCCCGGACAA	AAAATAACAT	CCAAAGATAT	240
TTTGGCACTA	ACAGTGTGAT	CTGTAGCAAG	AAAGATAAGC	AGTCTGTTCG	AACTGAGGAG	300
ACTTCCAAGG	AGACTTTCAGA	GAGCCAAGAC	AGTGAAGAGG	AAAATACGAA	AAAAGACTTG	360
TTAGGCATTA	TTAAGGGCAT	GAAAGTTGAA	TTAAGCACAG	TAAATGTACG	AACAACAAAG	420
CCCCCAAAA	GAAGACCACT	TAAAAGTTTG	GAAGCTACAC	TTGGCAGGCT	TCGAAGAGCT	480
ACAGAATATG	CTCCAAAGAA	GAGAATTGAG	CCCCTGAGTC	CTGAGTTGGT	GGCAGCTGCA	540
TCTGCTGTGG	CAGATTCTCT	CCCTTTTGAT	AAGCAACAA	CCAAGTCAGA	GCTGCTGAGC	600
CAGCTCCAGC	AGCATGAGGA	AGAGTCAAGG	GCACAGAGAG	ATGCAAGAGC	ACCTAAATTT	660
AGTTTCAGTA	ACATAATATC	AGATATGAAA	GTGCCCAGAT	CTGCTACAGC	TAGAGTTCTG	720
TCAAGACCAG	AGCTTCGGAT	TCAGTTTGAT	GAAGGCTATG	ACAATTATCC	TGGCCAGGAG	780
AAGACGGATG	ATCTTTAAAA	AAGGAAAAAT	ATATTTCACG	GGAAAAAGCT	TAATATTTTT	840
GACATGATGG	CAGTTACTAA	AGAAGCACTT	GAAACAGACA	CATCACCTTC	ACTTTGGGAT	900
GTGGAATTGG	CTAAGCACTT	AGCCACAGTA	AATGAACAC	CCCTTCAGAA	TGGATTTGAA	960
GAGCTGATCC	AGTGGACAAA	AGAGGGGAAA	CTATGGGAGT	TCCCAATTAA	CAATGAAGCA	1020
GGTTTGTGAT	ATGATGGTTC	AGAATTTCAT	GAACATATAT	TTCTGGGAGC	ACACCTGGAG	1080
AGAACTTCCAA	AACAAGGACC	AATTCGCCAC	TTTATGGAGC	TGGTGACTTG	TGGCCTTTCC	1140
AAAAATTCAT	ATCTTAGTGT	TAAACAGAA	GTTGAACACA	TAGAGTGGTT	TGAAATTTAT	1200
TTTAATGAAA	AAAAGGATAT	TCTAAAAGAA	AGTAACATAC	ACTTCAATTA	AGACCATGGA	1260
AATTTTATT	TCAAACAATT	AGAGATGGAT	ATTACAACTA	AATAAAATAA	TTGC	1314

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 1272669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Leu	His	Arg	Ile	Pro	Ala	Phe	Leu	Arg	Pro	Arg	Pro	Phe	Ser	Gly
1				5					10					15	
Leu	Pro	Leu	Ser	Cys	Gly	Asn	Arg	Asp	Val	Ser	Val	Ala	Val	Leu	Pro
			20					25					30		
Ala	Ala	Gln	Ser	Gly	Ala	Val	Arg	Thr	Glu	Asn	Asn	Ile	Gln	Arg	His
			35					40					45		
Phe	Cys	Thr	Ser	Arg	Ser	Ile	Cys	Ser	Lys	Lys	Val	Asp	Gln	Ser	Val
			50				55				60				
Pro	Ala	Asn	Glu	Ile	Ser	Gln	Lys	Ala	Ala	Glu	Ser	Gln	Gly	Arg	Gly
			65			70				75				80	
Lys	Glu	Thr	Leu	Lys	Lys	Asp	Leu	Leu	Asp	Ile	Ile	Lys	Asp	Met	Lys
			85						90					95	
Val	Asp	Leu	Ser	Thr	Ala	Asn	Val	Lys	Thr	Pro	Lys	Pro	Arg	Gly	Arg
			100					105					110		
Lys	Pro	Ser	Ala	Ser	Leu	Glu	Ala	Thr	Val	Asp	Arg	Leu	Gln	Lys	Ala
			115				120						125		
Pro	Glu	Asp	Pro	Pro	Lys	Arg	Asn	Glu	Phe	Leu	Ser	Pro	Glu	Leu	

PF-0385-1 DIV

130	135	140
Val Ala Ala Ala Ser	Ala Val Ala Asp Ser	Leu Pro Phe Asp Lys Gln
145	150	155
Thr Thr Lys Ser Glu	Leu Leu Arg Gln Leu	Gln His Glu Glu Glu
	165	170
Leu Arg Ala Gln Lys	Asp Arg Glu Lys Arg	Arg Ile Ser Phe Thr His
	180	185
Ile Ile Ser Asn Met	Lys Ile Ala Lys Ser	Pro Ser Gly Arg Ala Ser
	195	200
Thr Arg Pro Gln His	Gln Ile Gln Phe Asp	Glu Asp Met Asp Ser Ser
	210	215
Leu Lys Gln Glu Lys	Pro Thr Asp Phe Arg	Lys Arg Lys Tyr Leu Phe
225	230	235
Lys Gly Lys Arg Leu	Ser Ile Phe Ala Asp	Lys Ala Phe Ala Asp Glu
	245	250
Pro Pro Glu Pro Glu	Ala Ser Pro Ser Leu	Trp Glu Ile Glu Phe Ala
	260	265
Lys Gln Leu Ala Ser	Val Ala Asp Gln Pro	Phe Glu Asn Gly Phe Glu
	275	280
Glu Met Ile Gln Trp	Thr Lys Glu Gly Lys	Leu Trp Glu Phe Pro Val
290	295	300
Asn Asn Glu Ala Gly	Leu Asp Asp Asp Gly	Ser Glu Phe His Glu His
305	310	315
Ile Phe Leu Asp Lys	Tyr Leu Glu Asp Phe	Pro Lys Gln Gly Pro Ile
	325	330
Arg Leu Phe Met Glu	Leu Val Thr Cys Gly	Leu Ser Lys Asn Pro Tyr
	340	345
Leu Ser Val Lys Gln	Lys Val Glu His Ile	Glu Trp Phe Arg Asn Tyr
	355	360
Phe Asn Glu Lys Arg	Asp Ile Leu Lys Glu	Asn Ile Ala Phe Thr
370	375	380